STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information. Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: *10/048,116A*
Source: *1Fw116*
Date Processed by STIC: *12/29/05*

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
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2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
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MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE __CHECKER VERSION 4.2.2 PROGRAM__, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

> http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
   U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street. Alexandria. VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

ERROR DETECTED   **SUGGESTED CORRECTION**   SERIAL NUMBER: _10/048,116A_

1 ____ Wrapped Nucleics
Wrapped Aminos   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 ____ Invalid Line Length   The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ____ Misaligned Amino
Numbering   The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 ____ Non-ASCII   The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ____ Variable Length   Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ PatentIn 2.0
"bug"   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _2,4,6,8_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 ____ Skipped Sequences
(OLD RULES)   Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ____ Skipped Sequences
(NEW RULES)   Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 ____ Use of n's or Xaa's
(NEW RULES)   Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ____ Invalid <213>
Response   Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 ____ Use of <220>   Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 ____ PatentIn 2.0
"bug"   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____ Misuse of n/Xaa   "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid
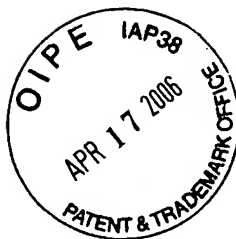
IFW16

RAW SEQUENCE LISTING   DATE: 12/29/2005
PATENT APPLICATION: US/10/048,116A TIME: 12:20:15

Input Set : A:\seq list.txt
Output Set: N:\CRF4\12292005\J048116A.raw

```
 3 <110> APPLICANT: CNRS
 5 <120> TITLE OF INVENTION: RECOMBINANT PROTEINS AND MOLECULAR COMPLEXES DERIVED
 6       FROM THESE PROTEINS, ANALOGOUS TO MOLECULES INVOLVED IN
 7       IMMUNE RESPONSES
 9 <130> FILE REFERENCE: 1721-47
11 <140> CURRENT APPLICATION NUMBER: 10/048,116A
12 <141> CURRENT FILING DATE: 2002-02-27
14 <150> PRIOR APPLICATION NUMBER: PCT/FR00/02193
15 <151> PRIOR FILING DATE: 2000-07-28
17 <150> PRIOR APPLICATION NUMBER: FR99/09862
18 <151> PRIOR FILING DATE: 1999-07-29
20 <160> NUMBER OF SEQ ID NOS: 8
22 <170> SOFTWARE: PatentIn Ver. 2.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 1517
26 <212> TYPE: DNA
27 <213> ORGANISM: Artificial Sequence
29 <220> FEATURE:
30 <223> OTHER INFORMATION: Description of Artificial Sequence: construct
31       coding IAalpha(d)/Fc
33 <220> FEATURE:
34 <221> NAME/KEY: CDS
35 <222> LOCATION: (18)..(1502)
37 <400> SEQUENCE: 1
38 aaggggggga attcagg atg ccg tgc agc aga gct ctg att ctg ggg gtc      50
39                     Met Pro Cys Ser Arg Ala Leu Ile Leu Gly Val
40                      1               5                  10
42 ctc gcc ctg aac acc atg ctc agc ctc tgc gga ggt gaa gac gac att     98
43 Leu Ala Leu Asn Thr Met Leu Ser Leu Cys Gly Gly Glu Asp Asp Ile
44              15                  20                  25
46 gag gcc gac cac gta ggc ttc tat ggt aca act gtt tat cag tct cct    146
47 Glu Ala Asp His Val Gly Phe Tyr Gly Thr Thr Val Tyr Gln Ser Pro
48              30                  35                  40
50 gga gac att ggc cag tac aca cat gaa ttt gat ggt gat gag ttg ttc    194
51 Gly Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly Asp Glu Leu Phe
52          45                  50                  55
54 tat gtg gac ttg gat aag aag aaa act gtc tgg agg ctt cct gag ttt    242
55 Tyr Val Asp Leu Asp Lys Lys Lys Thr Val Trp Arg Leu Pro Glu Phe
56   60                  65                  70                  75
58 ggc caa ttg ata ctc ttt gag ccc caa ggt gga ctg caa aac ata gct    290
59 Gly Gln Leu Ile Leu Phe Glu Pro Gln Gly Gly Leu Gln Asn Ile Ala
60                  80                  85                  90
62 gca gaa aaa cac aac ttg gga atc ttg act aag agg tca aat ttc acc    338
```

```
63 Ala Glu Lys His Asn Leu Gly Ile Leu Thr Lys Arg Ser Asn Phe Thr
64         95              100             105
66 cca gct acc aat gag gct cct caa gcg act gtg ttc ccc aag tcc cct    386
67 Pro Ala Thr Asn Glu Ala Pro Gln Ala Thr Val Phe Pro Lys Ser Pro
68         110             115             120
70 gtg ctg ctg ggt cag ccc aac acc ctt atc tgc ttt gtg gac aac atc    434
71 Val Leu Leu Gly Gln Pro Asn Thr Leu Ile Cys Phe Val Asp Asn Ile
72     125             130             135
74 ttc cca cct gtg atc aac atc aca tgg ctc aga aat agc aag tca gtc    482
75 Phe Pro Pro Val Ile Asn Ile Thr Trp Leu Arg Asn Ser Lys Ser Val
76 140             145             150             155
78 aca gac ggc gtt tat gag acc agc ttc ctc gtc aac cgt gac cat tcc    530
79 Thr Asp Gly Val Tyr Glu Thr Ser Phe Leu Val Asn Arg Asp His Ser
80                 160             165             170
82 ttc cac aag ctg tct tat ctc acc ttc atc cct tct gat gat gac att    578
83 Phe His Lys Leu Ser Tyr Leu Thr Phe Ile Pro Ser Asp Asp Asp Ile
84             175             180             185
86 tat gac tgc aag gtg gag cac tgg ggc ctg gag gag ccg gtt ctg aaa    626
87 Tyr Asp Cys Lys Val Glu His Trp Gly Leu Glu Glu Pro Val Leu Lys
88         190             195             200
90 cac tgg gaa cct gag att cca gcc ccc atg tca gag ctg aca gaa act    674
91 His Trp Glu Pro Glu Ile Pro Ala Pro Met Ser Glu Leu Thr Glu Thr
92     205             210             215
94 gga ggt gga gga tcc act aca gct cca tca gct cag ctc gaa aaa gag    722
95 Gly Gly Gly Gly Ser Thr Thr Ala Pro Ser Ala Gln Leu Glu Lys Glu
96 220             225             230             235
98 ctc cag gcc ctg gag aag gaa aat gca cag ctg gaa tgg gag ttg caa    770
99 Leu Gln Ala Leu Glu Lys Glu Asn Ala Gln Leu Glu Trp Glu Leu Gln
100             240             245             250
102 gca ctg gaa aag gaa ctg gct cag gca gca tct gag ccc aga ggg ccc    818
103 Ala Leu Glu Lys Glu Leu Ala Gln Ala Ala Ser Glu Pro Arg Gly Pro
104             255             260             265
106 aca atc aag ccc tgt cct cca tgc aaa tgc cca gca cct aac ctc ttg    866
107 Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu
108         270             275             280
110 ggt gga cca tcc gtc ttc atc ttc cct cca aag atc aag gat gta ctc    914
111 Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu
112     285             290             295
114 atg atc tcc ctg agc ccc ata gtc aca tgt gtg gtg gtg gat gtg agc    962
115 Met Ile Ser Leu Ser Pro Ile Val Thr Cys Val Val Val Asp Val Ser
116 300             305             310             315
118 gag gat gac cca gat gtc cag atc agc tgg ttt gtg aac aac gtg gaa   1010
119 Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu
120             320             325             330
122 gta cac aca gct cag aca caa acc cat aga gag gat tac aac agt act   1058
123 Val His Thr Ala Gln Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr
124             335             340             345
126 ctc cgg gtg gtc agt gcc ctc ccc atc cag cac cag gac tgg atg agt   1106
127 Leu Arg Val Val Ser Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser
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RAW SEQUENCE LISTING   DATE: 12/29/2005
PATENT APPLICATION: US/10/048,116A   TIME: 12:20:15

Input Set : A:\seq list.txt
Output Set: N:\CRF4\12292005\J048116A.raw

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128        350              355              360
130 ggc aag gag ttc aaa tgc aag gtc aac aac aaa gac ctc cca gcg ccc  1154
131 Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro
132    365              370              375
134 atc gag aga acc atc tca aaa ccc aaa ggg tca gta aga gct cca cag  1202
135 Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln
136 380              385              390              395
138 gta tat gtc ttg cct cca cca gaa gaa gag atg act aag aaa cag gtc  1250
139 Val Tyr Val Leu Pro Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val
140              400              405              410
142 act ctg acc tgc atg gtc aca gac ttc atg cct gaa gac att tac gtg  1298
143 Thr Leu Thr Cys Met Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val
144              415              420              425
146 gag tgg acc aac aac ggg aaa aca gag cta aac tac aag aac act gaa  1346
147 Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu
148    430              435              440
150 cca gtc ctg gac tct gat ggt tct tac ttc atg tac agc aag ctg aga  1394
151 Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg
152    445              450              455
154 gtg gaa aag aag aac tgg gtg gaa aga aat agc tac tcc tgt tca gtg  1442
155 Val Glu Lys Lys Asn Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val
156 460              465              470              475
158 gtc cac gag ggt ctg cac aat cac cac acg act aag agc ttc tcc cgg  1490
159 Val His Glu Gly Leu His Asn His His Thr Thr Lys Ser Phe Ser Arg
160              480              485              490
162 act ccg ggt aaa tgatgactcg acctg                                 1517
163 Thr Pro Gly Lys
164              495
167 <210> SEQ ID NO: 2
168 <211> LENGTH: 495
169 <212> TYPE: PRT
170 <213> ORGANISM: Artificial Sequence
172 <220> FEATURE:
172 <223> OTHER INFORMATION: see item 6 on Error Summary Sheet
172 <400> 2
173 Met Pro Cys Ser Arg Ala Leu Ile Leu Gly Val Leu Ala Leu Asn Thr
174 1              5              10              15
176 Met Leu Ser Leu Cys Gly Gly Glu Asp Asp Ile Glu Ala Asp His Val
177    20              25              30
179 Gly Phe Tyr Gly Thr Thr Val Tyr Gln Ser Pro Gly Asp Ile Gly Gln
180    35              40              45
182 Tyr Thr His Glu Phe Asp Gly Asp Glu Leu Phe Tyr Val Asp Leu Asp
183    50              55              60
185 Lys Lys Lys Thr Val Trp Arg Leu Pro Glu Phe Gly Gln Leu Ile Leu
186 65              70              75              80
188 Phe Glu Pro Gln Gly Gly Leu Gln Asn Ile Ala Ala Glu Lys His Asn
189              85              90              95
191 Leu Gly Ile Leu Thr Lys Arg Ser Asn Phe Thr Pro Ala Thr Asn Glu
192              100              105              110
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W--> (circled) marks at lines 172 <220>, 172 <223>, 172 <400> 2

Handwritten: see item 6 on Error Summary Sheet (same error in seqs. 4, 6, 8)

RAW SEQUENCE LISTING   DATE: 12/29/2005
PATENT APPLICATION: US/10/048,116A   TIME: 12:20:15

Input Set : A:\seq list.txt
Output Set: N:\CRF4\12292005\J048116A.raw

```
194 Ala Pro Gln Ala Thr Val Phe Pro Lys Ser Pro Val Leu Leu Gly Gln
195         115                 120                 125
197 Pro Asn Thr Leu Ile Cys Phe Val Asp Asn Ile Phe Pro Pro Val Ile
198     130                 135                 140
200 Asn Ile Thr Trp Leu Arg Asn Ser Lys Ser Val Thr Asp Gly Val Tyr
201 145                 150                 155                 160
203 Glu Thr Ser Phe Leu Val Asn Arg Asp His Ser Phe His Lys Leu Ser
204             165                 170                 175
206 Tyr Leu Thr Phe Ile Pro Ser Asp Asp Asp Ile Tyr Asp Cys Lys Val
207         180                 185                 190
209 Glu His Trp Gly Leu Glu Glu Pro Val Leu Lys His Trp Glu Pro Glu
210         195                 200                 205
212 Ile Pro Ala Pro Met Ser Glu Leu Thr Glu Thr Gly Gly Gly Gly Ser
213     210                 215                 220
215 Thr Thr Ala Pro Ser Ala Gln Leu Glu Lys Glu Leu Gln Ala Leu Glu
216 225                 230                 235                 240
218 Lys Glu Asn Ala Gln Leu Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu
219             245                 250                 255
221 Leu Ala Gln Ala Ala Ser Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys
222         260                 265                 270
224 Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val
225     275                 280                 285
227 Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser
228     290                 295                 300
230 Pro Ile Val Thr Cys Val Val Val Asp Val Ser Glu Asp Asp Pro Asp
231 305                 310                 315                 320
233 Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln
234             325                 330                 335
236 Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser
237         340                 345                 350
239 Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys
240     355                 360                 365
242 Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile
243     370                 375                 380
245 Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro
246 385                 390                 395                 400
248 Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met
249             405                 410                 415
251 Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn
252         420                 425                 430
254 Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser
255         435                 440                 445
257 Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn
258     450                 455                 460
260 Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu
261 465                 470                 475                 480
263 His Asn His His Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys
264             485                 490                 495
267 <210> SEQ ID NO: 3
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RAW SEQUENCE LISTING   DATE: 12/29/2005
PATENT APPLICATION: US/10/048,116A   TIME: 12:20:15

Input Set : A:\seq list.txt
Output Set: N:\CRF4\12292005\J048116A.raw

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268 <211> LENGTH: 1485
269 <212> TYPE: DNA
270 <213> ORGANISM: Artificial Sequence
272 <220> FEATURE:
273 <223> OTHER INFORMATION: Description of Artificial Sequence:coding region
274       of SEQ ID NO:1
276 <220> FEATURE:
277 <221> NAME/KEY: CDS
278 <222> LOCATION: (1)..(1485)
280 <400> SEQUENCE: 3
281 atg ccg tgc agc aga gct ctg att ctg ggg gtc ctc gcc ctg aac acc   48
282 Met Pro Cys Ser Arg Ala Leu Ile Leu Gly Val Leu Ala Leu Asn Thr
283  1               5                  10                  15
285 atg ctc agc ctc tgc gga ggt gaa gac gac att gag gcc gac cac gta   96
286 Met Leu Ser Leu Cys Gly Gly Glu Asp Asp Ile Glu Ala Asp His Val
287                 20                  25                  30
289 ggc ttc tat ggt aca act gtt tat cag tct cct gga gac att ggc cag  144
290 Gly Phe Tyr Gly Thr Thr Val Tyr Gln Ser Pro Gly Asp Ile Gly Gln
291             35                  40                  45
293 tac aca cat gaa ttt gat ggt gat gag ttg ttc tat gtg gac ttg gat  192
294 Tyr Thr His Glu Phe Asp Gly Asp Glu Leu Phe Tyr Val Asp Leu Asp
295         50                  55                  60
297 aag aag aaa act gtc tgg agg ctt cct gag ttt ggc caa ttg ata ctc  240
298 Lys Lys Lys Thr Val Trp Arg Leu Pro Glu Phe Gly Gln Leu Ile Leu
299  65                  70                  75                  80
301 ttt gag ccc caa ggt gga ctg caa aac ata gct gca gaa aaa cac aac  288
302 Phe Glu Pro Gln Gly Gly Leu Gln Asn Ile Ala Ala Glu Lys His Asn
303                 85                  90                  95
305 ttg gga atc ttg act aag agg tca aat ttc acc cca gct acc aat gag  336
306 Leu Gly Ile Leu Thr Lys Arg Ser Asn Phe Thr Pro Ala Thr Asn Glu
307                100                 105                 110
309 gct cct caa gcg act gtg ttc ccc aag tcc cct gtg ctg ctg ggt cag  384
310 Ala Pro Gln Ala Thr Val Phe Pro Lys Ser Pro Val Leu Leu Gly Gln
311            115                 120                 125
313 ccc aac acc ctt atc tgc ttt gtg gac aac atc ttc cca cct gtg atc  432
314 Pro Asn Thr Leu Ile Cys Phe Val Asp Asn Ile Phe Pro Pro Val Ile
315        130                 135                 140
317 aac atc aca tgg ctc aga aat agc aag tca gtc aca gac ggc gtt tat  480
318 Asn Ile Thr Trp Leu Arg Asn Ser Lys Ser Val Thr Asp Gly Val Tyr
319 145                 150                 155                 160
321 gag acc agc ttc ctc gtc aac cgt gac cat tcc ttc cac aag ctg tct  528
322 Glu Thr Ser Phe Leu Val Asn Arg Asp His Ser Phe His Lys Leu Ser
323                165                 170                 175
325 tat ctc acc ttc atc cct tct gat gat gac att tat gac tgc aag gtg  576
326 Tyr Leu Thr Phe Ile Pro Ser Asp Asp Asp Ile Tyr Asp Cys Lys Val
327            180                 185                 190
329 gag cac tgg ggc ctg gag gag ccg gtt ctg aaa cac tgg gaa cct gag  624
330 Glu His Trp Gly Leu Glu Glu Pro Val Leu Lys His Trp Glu Pro Glu
331            195                 200                 205
```

Input Set : **A:\seq list.txt**
Output Set: **N:\CRF4\12292005\J048116A.raw**

L:172 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:2, <213>
ORGANISM:Artificial Sequence
L:172 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:2, <213>
ORGANISM:Artificial Sequence
L:172 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:2,Line#:172
L:411 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:4, <213>
ORGANISM:Artificial Sequence
L:411 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:4, <213>
ORGANISM:Artificial Sequence
L:411 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:4,Line#:411
L:606 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:6, <213>
ORGANISM:Artificial Sequence
L:606 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:6, <213>
ORGANISM:Artificial Sequence
L:606 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:6,Line#:606
L:768 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:8, <213>
ORGANISM:Artificial Sequence
L:768 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:8, <213>
ORGANISM:Artificial Sequence
L:768 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:8,Line#:768